

SEQUENCE LISTING

<110> Mello, Craig C.
Tabara, Hiroaki
Grishok, Alla
Fire, Andrew

<120> RNA INTERFERENCE PATHWAY GENES AS TOOLS FOR TARGETED GENETIC INTERFERENCE

<130> UMY-052DV1

<140> US 09/689,992

<141> 2000-10-13

<150> US 60/193,218

<151> 2000-03-30

<150> US 60/159,776

<151> 1999-10-15

<160> 14

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3719

<212> DNA

<213> Caenorhabditis elegans

<400> 1

cagccacaaa	gtgatgaaac	atgtcctcga	attttcccga	attggaaaaa	ggattttatc	60
gtcatttctct	cgatccggtg	tgatcaatta	ttagcagcta	taagatatat	aagtttgata	120
ttaatattat	aggagatgaa	atggcttgcg	aggccactg	gtaaatgcga	cggcaaatc	180
tatgagaaga	aagtacttct	tttggtaaat	tggttcaagt	tctccagcaa	aatttacgat	240
cggaataact	acgagtatga	agtgaaaatg	acaaaggaag	tattgaatag	aaaaccagga	300
aaacctttcc	caaaaaagac	agaaattcca	atgtaagtgc	ttgtaaatta	gtcaaaacta	360
attttatttt	tcagtcccga	tcgtgcaaaa	ctcttctggc	aacatcttcg	gcatgagaag	420
aagcagacag	attttattct	cgaagactat	gtttttgatg	aaaaggacac	tgttttatagt	480
gtttgtcgac	tgaacactgt	cacatcaaaa	atgctggttt	cggagaaaag	agtaaaaaag	540
gattcggaga	aaaaagatga	aaaggatttg	gagaaaaaaa	tcttatacac	aatgatactt	600
acctatcgta	aaaaatttca	cctgaacttt	agtcgagaaa	atccggaaaa	agacgaagaa	660
gcgaatcgga	gttacaaatt	cctgaagggt	tatgaaaaac	acgcattata	acaaacaaaa	720
ttagctttca	gaatgttatg	accagaaaag	ttcgctacgc	gccttttggtg	aacgaggaga	780
ttaaagtgtg	agttgcaata	ataataataa	taatcacctc	aactcattta	tatatattta	840
gacaattcgc	gaaaaatttt	gtgtacgata	ataattcaat	tctgcgagtt	cctgaatcgt	900
ttcacgatcc	aaacagattc	gaacaatcat	tagaagtagc	accaagaatc	gaagcatggt	960
ttggaattta	cattggaatc	aaagaattgt	tcgatgggtga	acctgtgctc	aattttgcaa	1020
gtaagtttga	gaaactgcga	taaaaaatca	tgtgattttt	gttgaaagttg	tcgataaaact	1080
attctacaat	gcaccgaaaa	tgtctcttct	ggattatctt	ctcctaattg	tcgaccccca	1140
gtcgtgtaac	gatgatgtac	gaaaagatct	taaaacaaaa	ctgatggcgg	gaaaaatgac	1200
aatcagacaa	gccgcgcggc	caagaattcg	acaattattg	gaaaatttga	agctgaaatg	1260
cgcagaagtt	tgggataacg	aaatgttagt	ttaaattatt	caaacaatta	atatacaaat	1320
tgattttcag	gtcgagattg	acagaacgac	atctgacatt	tctagatttg	tgcgaggaaa	1380
actctcttgt	ttataaagtc	actggtaaat	cggacagagg	aagaaatgca	aaaaagtacg	1440
atactacatt	gttcaaaatc	tatgaggaaa	acaaaaagtt	cattgagttt	ccccacctac	1500
cactagtcaa	agttaaaagt	ggagcaaaaag	aatacgcgtg	accaatggaa	catcttgaa	1560
ttcatgagaa	gccacaaaga	tacaagaatc	gaattgatct	ggtgatgcaa	gacaagtttc	1620
taaagcgagc	tacacgaaaa	cctcacgact	acaaagaaaa	taccctaaaa	atgctgaaag	1680
aattggattt	ctcttctgaa	gagctaaatt	ttgttgaaag	atttgatta	tgctccaaac	1740
ttcagatgat	cgaatgtcca	gaaaggttt	tgaaagagcc	aatgcttggtg	aatagtgtaa	1800

```

atgaacaaat taaaatgaca ccagtgattc gtggatttca agaaaaacaa ttgaatgtgg 1860
ttcccgaaaa agaactttgc tgtgctgttt ttgtagtcaa cgaacacagc ggaaatccat 1920
gcttagaaga gaacgacggt gtgtaagtgt tttctacgta gattattccg aaatattttc 1980
agtaagtctt acaccgaact aattgggtgt tgcaagtcc gtggaatacg aattgggtgcc 2040
aatgaaaaca gaggagcgca atctattatg tacgacgcga cgaaaaatga atatgccgta 2100
agtttcagaa aattgaaagt ttttaaatat catatttaca gttctacaaa aattgtacac 2160
taaataccgg aatcggtaga tttgaaatag ccgcaacaga agcgaagaat atgtttgaac 2220
gtcttccgga taaagaacaa aaagtcttaa tgttcattat catttccaaa cgacaactga 2280
atgcttacgg ttttgtgaaa cattattgcg atcacaccat cgggtgtagct aatcagcata 2340
ttacttctga aacagtcaca aaagctttgg catcactaag gcacgagaaa ggatcaaaac 2400
gaattttcta tcaaattgca ttgaaaatca acgcgaaatt aggagggtatt aaccaggagc 2460
ttgactggtc agaaattgca gaaatatcac cagaagaaaa agaaagacgg aaaacaatgc 2520
cattaactat gtatgttgga attgatgtaa ctcatccaac ctctacagt ggaattgatt 2580
attctatagc ggctgtagta gcgagtatca atccaggtgg aactatctat cgaaatatga 2640
ttgtgactca agaagaatgt cgtcccgggtg agcgtgcagt ggctcatgga cgggaaagaa 2700
cagatathtt ggaagcaaag ttcgtgaaat tgctcagaga attcgcagaa gtgagttgtc 2760
ttgagtattt aaaagatctc tgggattttt aatttttttg taaactttca gaacaacgac 2820
aatcgagcac cagcgcatat tgtagtctat cgagacggag ttagcgattc ggagatgcta 2880
cgtgttagtc atgatgagct tcatcttta aaaagcgaag taaaacaatt catgtcggaa 2940
cgggatggag aagatccaga gccgaagtac acgttcattg tgattcagaa aagacacaat 3000
acacgattgc ttgaagaat ggaaaaagat aagccagtg tcaataaaga tcttactcct 3060
gctgaaacag atgtcgctgt tgctgctgtt aaacaatggg aggaggatat gaaagaaagc 3120
aaagaaaactg gaattgtgaa cccatcatcc ggaacaactg tggataaact tatcgtttcg 3180
aaatacaaat tcgatttttt cttggcatct catcatggtg tccttggtac atctcgtcca 3240
ggacattaca ctgttatgta tgacgataaa ggaatgagcc aagatgaagt ctatgtaagc 3300
gttttgtaata gcagttagcg attttaggat tttgtaatcc gcatatagtt attataaaaa 3360
aatgtttcag aaaatgacct acggacttgc ttttctctct gctagatgtc gaaaacccat 3420
ctcgttgctt gttccggttc attatgctca tttatcatgt gaaaaagcga aagagcttta 3480
tcgaacttac aaggaacatt acatcgggtg ctatgcacag ccacggactc gcacagaaat 3540
ggaacatttt ctccaaacta acgtgaagta ccctggaatg tcgttcgcat aacattttgc 3600
aaaagtgtcg cccgtttcaa tcaaattttt caattgtaga tattgtactt actttttttt 3660
aaagcccggg ttcaaaaatt cattccatga ctaacgtttt cataaattac ttgaaattt 3719

```

<210> 2
 <211> 3227
 <212> DNA
 <213> *Caenorhabditis elegans*

<220>
 <221> CDS
 <222> (21)...(3080)

```

<400> 2
cagccacaaa gtgatgaaac atg tcc tcg aat ttt ccc gaa ttg gaa aaa gga 53
                Met Ser Ser Asn Phe Pro Glu Leu Glu Lys Gly
                1             5             10

ttt tat cgt cat tct ctc gat ccg gag atg aaa tgg ctt gcg agg ccc 101
Phe Tyr Arg His Ser Leu Asp Pro Glu Met Lys Trp Leu Ala Arg Pro
                15             20             25

act ggt aaa tgc gac ggc aaa ttc tat gag aag aaa gta ctt ctt ttg 149
Thr Gly Lys Cys Asp Gly Lys Phe Tyr Glu Lys Lys Val Leu Leu Leu
                30             35             40

gta aat tgg ttc aag ttc tcc agc aaa att tac gat cgg gaa tac tac 197
Val Asn Trp Phe Lys Phe Ser Ser Lys Ile Tyr Asp Arg Glu Tyr Tyr
                45             50             55

gag tat gaa gtg aaa atg aca aag gaa gta ttg aat aga aaa cca gga 245
Glu Tyr Glu Val Lys Met Thr Lys Glu Val Leu Asn Arg Lys Pro Gly

```

60	65	70	75	
aaa cct ttc cca aaa aag aca gaa att cca att ccc gat cgt gca aaa Lys Pro Phe Pro Lys Lys Thr Glu Ile Pro Ile Pro Asp Arg Ala Lys	80	85	90	293
ctc ttc tgg caa cat ctt cgg cat gag aag aag cag aca gat ttt att Leu Phe Trp Gln His Leu Arg His Glu Lys Lys Gln Thr Asp Phe Ile	95	100	105	341
ctc gaa gac tat gtt ttt gat gaa aag gac act gtt tat agt gtt tgt Leu Glu Asp Tyr Val Phe Asp Glu Lys Asp Thr Val Tyr Ser Val Cys	110	115	120	389
cga ctg aac act gtc aca tca aaa atg ctg gtt tcg gag aaa gta gta Arg Leu Asn Thr Val Thr Ser Lys Met Leu Val Ser Glu Lys Val Val	125	130	135	437
aaa aag gat tcg gag aaa aaa gat gaa aag gat ttg gag aaa aaa atc Lys Lys Asp Ser Glu Lys Lys Asp Glu Lys Asp Leu Glu Lys Lys Ile	140	145	150	485
tta tac aca atg ata ctt acc tat cgt aaa aaa ttt cac ctg aac ttt Leu Tyr Thr Met Ile Leu Thr Tyr Arg Lys Lys Phe His Leu Asn Phe	160	165	170	533
agt cga gaa aat ccg gaa aaa gac gaa gaa gcg aat cgg agt tac aaa Ser Arg Glu Asn Pro Glu Lys Asp Glu Glu Ala Asn Arg Ser Tyr Lys	175	180	185	581
ttc ctg aag aat gtt atg acc cag aaa gtt cgc tac gcg cct ttt gtg Phe Leu Lys Asn Val Met Thr Gln Lys Val Arg Tyr Ala Pro Phe Val	190	195	200	629
aac gag gag att aaa gta caa ttc gcg aaa aat ttt gtg tac gat aat Asn Glu Glu Ile Lys Val Gln Phe Ala Lys Asn Phe Val Tyr Asp Asn	205	210	215	677
aat tca att ctg cga gtt cct gaa tcg ttt cac gat cca aac aga ttc Asn Ser Ile Leu Arg Val Pro Glu Ser Phe His Asp Pro Asn Arg Phe	220	225	230	725
gaa caa tca tta gaa gta gca cca aga atc gaa gca tgg ttt gga att Glu Gln Ser Leu Glu Val Ala Pro Arg Ile Glu Ala Trp Phe Gly Ile	240	245	250	773
tac att gga atc aaa gaa ttg ttc gat ggt gaa cct gtg ctc aat ttt Tyr Ile Gly Ile Lys Glu Leu Phe Asp Gly Glu Pro Val Leu Asn Phe	255	260	265	821
gca att gtc gat aaa cta ttc tac aat gca ccg aaa atg tct ctt ctg Ala Ile Val Asp Lys Leu Phe Tyr Asn Ala Pro Lys Met Ser Leu Leu	270	275	280	869
gat tat ctt ctc cta att gtc gac ccc cag tcg tgt aac gat gat gta Asp Tyr Leu Leu Leu Ile Val Asp Pro Gln Ser Cys Asn Asp Asp Val	285	290	295	917
cga aaa gat ctt aaa aca aaa ctg atg gcg gga aaa atg aca atc aga Arg Lys Asp Leu Lys Thr Lys Leu Met Ala Gly Lys Met Thr Ile Arg	300	305	310	965

caa gcc gcg cgg cca aga att cga caa tta ttg gaa aat ttg aag ctg Gln Ala Ala Arg Pro Arg Ile Arg Gln Leu Leu Glu Asn Leu Lys Leu 320 325 330	1013
aaa tgc gca gaa gtt tgg gat aac gaa atg tcg aga ttg aca gaa cga Lys Cys Ala Glu Val Trp Asp Asn Glu Met Ser Arg Leu Thr Glu Arg 335 340 345	1061
cat ctg aca ttt cta gat ttg tgc gag gaa aac tct ctt gtt tat aaa His Leu Thr Phe Leu Asp Leu Cys Glu Glu Asn Ser Leu Val Tyr Lys 350 355 360	1109
gtc act ggt aaa tcg gac aga gga aga aat gca aaa aag tac gat act Val Thr Gly Lys Ser Asp Arg Gly Arg Asn Ala Lys Lys Tyr Asp Thr 365 370 375	1157
aca ttg ttc aaa atc tat gag gaa aac aaa aag ttc att gag ttt ccc Thr Leu Phe Lys Ile Tyr Glu Glu Asn Lys Lys Phe Ile Glu Phe Pro 380 385 390 395	1205
cac cta cca cta gtc aaa gtt aaa agt gga gca aaa gaa tac gct gta His Leu Pro Leu Val Lys Val Lys Ser Gly Ala Lys Glu Tyr Ala Val 400 405 410	1253
cca atg gaa cat ctt gaa gtt cat gag aag cca caa aga tac aag aat Pro Met Glu His Leu Glu Val His Glu Lys Pro Gln Arg Tyr Lys Asn 415 420 425	1301
cga att gat ctg gtg atg caa gac aag ttt cta aag cga gct aca cga Arg Ile Asp Leu Val Met Gln Asp Lys Phe Leu Lys Arg Ala Thr Arg 430 435 440	1349
aaa cct cac gac tac aaa gaa aat acc cta aaa atg ctg aaa gaa ttg Lys Pro His Asp Tyr Lys Glu Asn Thr Leu Lys Met Leu Lys Glu Leu 445 450 455	1397
gat ttc tct tct gaa gag cta aat ttt gtt gaa aga ttt gga tta tgc Asp Phe Ser Ser Glu Glu Leu Asn Phe Val Glu Arg Phe Gly Leu Cys 460 465 470 475	1445
tcc aaa ctt cag atg atc gaa tgt cca gga aag gtt ttg aaa gag cca Ser Lys Leu Gln Met Ile Glu Cys Pro Gly Lys Val Leu Lys Glu Pro 480 485 490	1493
atg ctt gtg aat agt gta aat gaa caa att aaa atg aca cca gtg att Met Leu Val Asn Ser Val Asn Glu Gln Ile Lys Met Thr Pro Val Ile 495 500 505	1541
cgt gga ttt caa gaa aaa caa ttg aat gtg gtt ccc gaa aaa gaa ctt Arg Gly Phe Gln Glu Lys Gln Leu Asn Val Val Pro Glu Lys Glu Leu 510 515 520	1589
tgc tgt gct gtt ttt gta gtc aac gaa aca gcg gga aat cca tgc tta Cys Cys Ala Val Phe Val Val Asn Glu Thr Ala Gly Asn Pro Cys Leu 525 530 535	1637
gaa gag aac gac gtt gtt aag ttc tac acc gaa cta att ggt ggt tgc Glu Glu Asn Asp Val Val Lys Phe Tyr Thr Glu Leu Ile Gly Gly Cys 540 545 550 555	1685

aag ttc cgt gga ata cga att ggt gcc aat gaa aac aga gga gcg caa Lys Phe Arg Gly Ile Arg Ile Gly Ala Asn Glu Asn Arg Gly Ala Gln 560 565 570	1733
tct att atg tac gac gcg acg aaa aat gaa tat gcc ttc tac aaa aat Ser Ile Met Tyr Asp Ala Thr Lys Asn Glu Tyr Ala Phe Tyr Lys Asn 575 580 585	1781
tgt aca cta aat acc gga atc ggt aga ttt gaa ata gcc gca aca gaa Cys Thr Leu Asn Thr Gly Ile Gly Arg Phe Glu Ile Ala Ala Thr Glu 590 595 600	1829
gcg aag aat atg ttt gaa cgt ctt ccc gat aaa gaa caa aaa gtc tta Ala Lys Asn Met Phe Glu Arg Leu Pro Asp Lys Glu Gln Lys Val Leu 605 610 615	1877
atg ttc att atc att tcc aaa cga caa ctg aat gct tac ggt ttt gtg Met Phe Ile Ile Ile Ser Lys Arg Gln Leu Asn Ala Tyr Gly Phe Val 620 625 630 635	1925
aaa cat tat tgc gat cac acc atc ggt gta gct aat cag cat att act Lys His Tyr Cys Asp His Thr Ile Gly Val Ala Asn Gln His Ile Thr 640 645 650	1973
tct gaa aca gtc aca aaa gct ttg gca tca cta agg cac gag aaa gga Ser Glu Thr Val Thr Lys Ala Leu Ala Ser Leu Arg His Glu Lys Gly 655 660 665	2021
tca aaa cga att ttc tat caa att gca ttg aaa atc aac gcg aaa tta Ser Lys Arg Ile Phe Tyr Gln Ile Ala Leu Lys Ile Asn Ala Lys Leu 670 675 680	2069
gga ggt att aac cag gag ctt gac tgg tca gaa att gca gaa ata tca Gly Gly Ile Asn Gln Glu Leu Asp Trp Ser Glu Ile Ala Glu Ile Ser 685 690 695	2117
cca gaa gaa aaa gaa aga cgg aaa aca atg cca tta act atg tat gtt Pro Glu Glu Lys Glu Arg Arg Lys Thr Met Pro Leu Thr Met Tyr Val 700 705 710 715	2165
gga att gat gta act cat cca acc tcc tac agt gga att gat tat tct Gly Ile Asp Val Thr His Pro Thr Ser Tyr Ser Gly Ile Asp Tyr Ser 720 725 730	2213
ata gcg gct gta gta gcg agt atc aat cca ggt gga act atc tat cga Ile Ala Ala Val Val Ala Ser Ile Asn Pro Gly Gly Thr Ile Tyr Arg 735 740 745	2261
aat atg att gtg act caa gaa gaa tgt cgt ccc ggt gag cgt gca gtg Asn Met Ile Val Thr Gln Glu Glu Cys Arg Pro Gly Glu Arg Ala Val 750 755 760	2309
gct cat gga cgg gaa aga aca gat att ttg gaa gca aag ttc gtg aaa Ala His Gly Arg Glu Arg Thr Asp Ile Leu Glu Ala Lys Phe Val Lys 765 770 775	2357
ttg ctc aga gaa ttc gca gaa aac aac gac aat cga gca cca gcg cat Leu Leu Arg Glu Phe Ala Glu Asn Asn Asp Asn Arg Ala Pro Ala His 780 785 790 795	2405
att gta gtc tat cga gac gga gtt agc gat tcg gag atg cta cgt gtt	2453

Ile Val Val Tyr Arg Asp Gly Val Ser Asp Ser Glu Met Leu Arg Val	
800 805 810	
agt cat gat gag ctt cga tct tta aaa agc gaa gta aaa caa ttc atg	2501
Ser His Asp Glu Leu Arg Ser Leu Lys Ser Glu Val Lys Gln Phe Met	
815 820 825	
tcg gaa cgg gat gga gaa gat cca gag ccg aag tac acg ttc att gtg	2549
Ser Glu Arg Asp Gly Glu Asp Pro Glu Pro Lys Tyr Thr Phe Ile Val	
830 835 840	
att cag aaa aga cac aat aca cga ttg ctt cga aga atg gaa aaa gat	2597
Ile Gln Lys Arg His Asn Thr Arg Leu Leu Arg Arg Met Glu Lys Asp	
845 850 855	
aag cca gtg gtc aat aaa gat ctt act cct gct gaa aca gat gtc gct	2645
Lys Pro Val Val Asn Lys Asp Leu Thr Pro Ala Glu Thr Asp Val Ala	
860 865 870 875	
gtt gct gct gtt aaa caa tgg gag gag gat atg aaa gaa agc aaa gaa	2693
Val Ala Ala Val Lys Gln Trp Glu Glu Asp Met Lys Glu Ser Lys Glu	
880 885 890	
act gga att gtg aac cca tca tcc gga aca act gtg gat aaa ctt atc	2741
Thr Gly Ile Val Asn Pro Ser Ser Gly Thr Thr Val Asp Lys Leu Ile	
895 900 905	
gtt tcg aaa tac aaa ttc gat ttt ttc ttg gca tct cat cat ggt gtc	2789
Val Ser Lys Tyr Lys Phe Asp Phe Phe Leu Ala Ser His His Gly Val	
910 915 920	
ctt ggt aca tct cgt cca gga cat tac act gtt atg tat gac gat aaa	2837
Leu Gly Thr Ser Arg Pro Gly His Tyr Thr Val Met Tyr Asp Asp Lys	
925 930 935	
gga atg agc caa gat gaa gtc tat aaa atg acc tac gga ctt gct ttt	2885
Gly Met Ser Gln Asp Glu Val Tyr Lys Met Thr Tyr Gly Leu Ala Phe	
940 945 950 955	
ctc tct gct aga tgt cga aaa ccc atc tcg ttg cct gtt ccg gtt cat	2933
Leu Ser Ala Arg Cys Arg Lys Pro Ile Ser Leu Pro Val Pro Val His	
960 965 970	
tat gct cat tta tca tgt gaa aaa gcg aaa gag ctt tat cga act tac	2981
Tyr Ala His Leu Ser Cys Glu Lys Ala Lys Glu Leu Tyr Arg Thr Tyr	
975 980 985	
aag gaa cat tac atc ggt gac tat gca cag cca cgg act cga cac gaa	3029
Lys Glu His Tyr Ile Gly Asp Tyr Ala Gln Pro Arg Thr Arg His Glu	
990 995 1000	
atg gaa cat ttt ctc caa act aac gtg aag tac cct gga atg tcg ttc	3077
Met Glu His Phe Leu Gln Thr Asn Val Lys Tyr Pro Gly Met Ser Phe	
1005 1010 1015	
gca taacattttg caaaagtgtc gcccgtttca atcaaatttt tcaattgtag	3130
Ala	
1020	
atattgtact tacttttttt taaagcccg tttcaaaaat tcattccatg actaacgttt	3190

tcataaatta cttgaaattt aaaaaaaaaa aaaaaaa

3227

<210> 3

<211> 1020

<212> PRT

<213> Caenorhabditis elegans

<400> 3

Met	Ser	Ser	Asn	Phe	Pro	Glu	Leu	Glu	Lys	Gly	Phe	Tyr	Arg	His	Ser
1				5					10					15	
Leu	Asp	Pro	Glu	Met	Lys	Trp	Leu	Ala	Arg	Pro	Thr	Gly	Lys	Cys	Asp
			20					25					30		
Gly	Lys	Phe	Tyr	Glu	Lys	Lys	Val	Leu	Leu	Leu	Val	Asn	Trp	Phe	Lys
		35					40					45			
Phe	Ser	Ser	Lys	Ile	Tyr	Asp	Arg	Glu	Tyr	Tyr	Glu	Tyr	Glu	Val	Lys
	50				55					60					
Met	Thr	Lys	Glu	Val	Leu	Asn	Arg	Lys	Pro	Gly	Lys	Pro	Phe	Pro	Lys
65					70					75					80
Lys	Thr	Glu	Ile	Pro	Ile	Pro	Asp	Arg	Ala	Lys	Leu	Phe	Trp	Gln	His
				85					90					95	
Leu	Arg	His	Glu	Lys	Lys	Gln	Thr	Asp	Phe	Ile	Leu	Glu	Asp	Tyr	Val
			100					105					110		
Phe	Asp	Glu	Lys	Asp	Thr	Val	Tyr	Ser	Val	Cys	Arg	Leu	Asn	Thr	Val
		115					120					125			
Thr	Ser	Lys	Met	Leu	Val	Ser	Glu	Lys	Val	Val	Lys	Lys	Asp	Ser	Glu
	130						135					140			
Lys	Lys	Asp	Glu	Lys	Asp	Leu	Glu	Lys	Lys	Ile	Leu	Tyr	Thr	Met	Ile
145					150					155					160
Leu	Thr	Tyr	Arg	Lys	Lys	Phe	His	Leu	Asn	Phe	Ser	Arg	Glu	Asn	Pro
				165					170					175	
Glu	Lys	Asp	Glu	Glu	Ala	Asn	Arg	Ser	Tyr	Lys	Phe	Leu	Lys	Asn	Val
			180					185					190		
Met	Thr	Gln	Lys	Val	Arg	Tyr	Ala	Pro	Phe	Val	Asn	Glu	Glu	Ile	Lys
		195					200					205			
Val	Gln	Phe	Ala	Lys	Asn	Phe	Val	Tyr	Asp	Asn	Asn	Ser	Ile	Leu	Arg
	210					215					220				
Val	Pro	Glu	Ser	Phe	His	Asp	Pro	Asn	Arg	Phe	Glu	Gln	Ser	Leu	Glu
225					230					235					240
Val	Ala	Pro	Arg	Ile	Glu	Ala	Trp	Phe	Gly	Ile	Tyr	Ile	Gly	Ile	Lys
				245					250					255	
Glu	Leu	Phe	Asp	Gly	Glu	Pro	Val	Leu	Asn	Phe	Ala	Ile	Val	Asp	Lys
			260					265					270		
Leu	Phe	Tyr	Asn	Ala	Pro	Lys	Met	Ser	Leu	Leu	Asp	Tyr	Leu	Leu	Leu
		275					280						285		
Ile	Val	Asp	Pro	Gln	Ser	Cys	Asn	Asp	Asp	Val	Arg	Lys	Asp	Leu	Lys
	290					295						300			
Thr	Lys	Leu	Met	Ala	Gly	Lys	Met	Thr	Ile	Arg	Gln	Ala	Ala	Arg	Pro
305					310					315					320
Arg	Ile	Arg	Gln	Leu	Glu	Asn	Leu	Lys	Leu	Lys	Cys	Ala	Glu	Val	
				325					330				335		
Trp	Asp	Asn	Glu	Met	Ser	Arg	Leu	Thr	Glu	Arg	His	Leu	Thr	Phe	Leu
			340					345					350		
Asp	Leu	Cys	Glu	Glu	Asn	Ser	Leu	Val	Tyr	Lys	Val	Thr	Gly	Lys	Ser
		355					360					365			
Asp	Arg	Gly	Arg	Asn	Ala	Lys	Lys	Tyr	Asp	Thr	Thr	Leu	Phe	Lys	Ile
	370					375						380			
Tyr	Glu	Glu	Asn	Lys	Lys	Phe	Ile	Glu	Phe	Pro	His	Leu	Pro	Leu	Val
385					390					395					400
Lys	Val	Lys	Ser	Gly	Ala	Lys	Glu	Tyr	Ala	Val	Pro	Met	Glu	His	Leu
				405					410					415	
Glu	Val	His	Glu	Lys	Pro	Gln	Arg	Tyr	Lys	Asn	Arg	Ile	Asp	Leu	Val


```

Phe Asp Phe Phe Leu Ala Ser His His Gly Val Leu Gly Thr Ser Arg
    915          920          925
Pro Gly His Tyr Thr Val Met Tyr Asp Asp Lys Gly Met Ser Gln Asp
    930          935          940
Glu Val Tyr Lys Met Thr Tyr Gly Leu Ala Phe Leu Ser Ala Arg Cys
    945          950          955          960
Arg Lys Pro Ile Ser Leu Pro Val Pro Val His Tyr Ala His Leu Ser
    965          970          975
Cys Glu Lys Ala Lys Glu Leu Tyr Arg Thr Tyr Lys Glu His Tyr Ile
    980          985          990
Gly Asp Tyr Ala Gln Pro Arg Thr Arg His Glu Met Glu His Phe Leu
    995          1000          1005
Gln Thr Asn Val Lys Tyr Pro Gly Met Ser Phe Ala
    1010          1015          1020

```

```

<210> 4
<211> 1222
<212> DNA
<213> Caenorhabditis elegans

```

```

<400> 4
atggatttaa ccaaactaac gtttgaaagc gttttcgggtg gatcagatgt tcctatgaag      60
ccttcccgat cggaggataa caaaacgcca agaaacagaa cagatttggg gatgtttctg      120
aagaaaactc ccctcatggt actagaagag gctgctaagg ctgtctatca aaagacgcca      180
acttggggca ctgtcgaact tcctgaaggc ttcgagatga cgttgattct gaatgaaatt      240
actgtaaaag gccaggcaac aagcaagaaa gctgcgagac aaaaggctgc tgttgaatat      300
ttacgcaagg ttgtggagaa aggaaagcac gaaatctttt tcattcctgg aacaacccaa      360
gaagaagctc tttcgaatat tgatcaaata tcggataagg ctgaggaatt gaaacgatca      420
acttcagatg ctgttcagga taacgataac gatgattcga ttcctacaag tgctgaattt      480
ccacctggta tttcgccaac cgagaattgg gtcggaaaagt tgcaggaaaa atctcaaaaa      540
agcaagctgc aagccccaat ctatgaagat tccaagaatg agagaaccga gcgtttcttg      600
gttatatgca cgatgtgcaa tcaaaaaacc agaggaatca gaagtaagaa gaaggacgca      660
aagaatcttg cagcatggtt gatgtggaaa gcgttggaag acggtatcga atctctggaa      720
tcatatgata tggttgatgt gattgaaaat ttggaagaag ctgaacattt actcgaaatt      780
caggatcaag catccaagat taaagacaag cattccgcac tgattgatat actctcggac      840
aagaaaagat tttcagacta cagcatggat ttcaacgtat tatcagttag cacaatggga      900
atacatcagg tgctattgga aatctcgttc cggcgtctag tttctccaga ccccgacgat      960
ttggaatagg gagcagaaca caccagact gaagaaatta tgaaggctac tgccgagaag     1020
gaaaagctac ggaagaagaa tatgccagat tccggggccgc tagtgtttgc tggacatggt     1080
tcatcggcgg aagaggctaa acagtgtgct tgtaaatacgg cgattatcca tttcaacacc     1140
tatgatttca cggattgaaa atattattgc gtattcctga aaaatgaagc gtctgaatga     1200
ttataaaaaa aaaaaaaaaa aa

```

```

<210> 5
<211> 407
<212> PRT
<213> Caenorhabditis elegans

```

```

<220>
<221> VARIANT
<222> (1)...(407)
<223> Xaa = Any Amino Acid

```

```

<400> 5
Met Asp Leu Thr Lys Leu Thr Phe Glu Ser Val Phe Gly Gly Ser Asp
    1          5          10          15
Val Pro Met Lys Pro Ser Arg Ser Glu Asp Asn Lys Thr Pro Arg Asn
    20          25          30
Arg Thr Asp Leu Glu Met Phe Leu Lys Lys Thr Pro Leu Met Val Leu
    35          40          45
Glu Glu Ala Ala Lys Ala Val Tyr Gln Lys Thr Pro Thr Trp Gly Thr

```

50	55	60																	
Val	Glu	Leu	Pro	Glu	Gly	Phe	Glu	Met	Thr	Leu	Ile	Leu	Asn	Glu	Ile				
65					70					75					80				
Thr	Val	Lys	Gly	Gln	Ala	Thr	Ser	Lys	Lys	Ala	Ala	Arg	Gln	Lys	Ala				
				85					90					95					
Ala	Val	Glu	Tyr	Leu	Arg	Lys	Val	Val	Glu	Lys	Gly	Lys	His	Glu	Ile				
		100						105					110						
Phe	Phe	Ile	Pro	Gly	Thr	Thr	Lys	Glu	Glu	Ala	Leu	Ser	Asn	Ile	Asp				
		115					120					125							
Gln	Ile	Ser	Asp	Lys	Ala	Glu	Glu	Leu	Lys	Arg	Ser	Thr	Ser	Asp	Ala				
	130					135				140									
Val	Gln	Asp	Asn	Asp	Asn	Asp	Asp	Ser	Ile	Pro	Thr	Ser	Ala	Glu	Phe				
145					150				155					160					
Pro	Pro	Gly	Ile	Ser	Pro	Thr	Glu	Asn	Trp	Val	Gly	Lys	Leu	Gln	Glu				
			165					170					175						
Lys	Ser	Gln	Lys	Ser	Lys	Leu	Gln	Ala	Pro	Ile	Tyr	Glu	Asp	Ser	Lys				
		180					185					190							
Asn	Glu	Arg	Thr	Glu	Arg	Phe	Leu	Val	Ile	Cys	Thr	Met	Cys	Asn	Gln				
	195					200				205									
Lys	Thr	Arg	Gly	Ile	Arg	Ser	Lys	Lys	Lys	Asp	Ala	Lys	Asn	Leu	Ala				
	210					215				220									
Ala	Trp	Leu	Met	Trp	Lys	Ala	Leu	Glu	Asp	Gly	Ile	Glu	Ser	Leu	Glu				
225				230					235					240					
Ser	Tyr	Asp	Met	Val	Asp	Val	Ile	Glu	Asn	Leu	Glu	Glu	Ala	Glu	His				
			245					250					255						
Leu	Leu	Glu	Ile	Gln	Asp	Gln	Ala	Ser	Lys	Ile	Lys	Asp	Lys	His	Ser				
		260					265					270							
Ala	Leu	Ile	Asp	Ile	Leu	Ser	Asp	Lys	Lys	Arg	Phe	Ser	Asp	Tyr	Ser				
	275						280				285								
Met	Asp	Phe	Asn	Val	Leu	Ser	Val	Ser	Thr	Met	Gly	Ile	His	Gln	Val				
	290					295				300									
Leu	Leu	Glu	Ile	Ser	Phe	Arg	Arg	Leu	Val	Ser	Pro	Asp	Pro	Asp	Asp				
305					310				315					320					
Leu	Glu	Met	Gly	Ala	Glu	His	Thr	Gln	Thr	Glu	Glu	Ile	Met	Lys	Ala				
			325					330					335						
Thr	Ala	Glu	Lys	Glu	Lys	Leu	Arg	Lys	Lys	Asn	Met	Pro	Asp	Ser	Gly				
		340					345					350							
Pro	Leu	Val	Phe	Ala	Gly	His	Gly	Ser	Ser	Ala	Glu	Glu	Ala	Lys	Gln				
	355						360				365								
Cys	Ala	Cys	Lys	Ser	Ala	Ile	Ile	His	Phe	Asn	Thr	Tyr	Asp	Phe	Thr				
	370				375				380										
Asp	Xaa	Lys	Tyr	Tyr	Cys	Val	Phe	Leu	Lys	Asn	Glu	Ala	Ser	Glu	Xaa				
385					390				395					400					
Leu	Xaa	Lys	Lys	Lys	Lys	Lys													
				405															

<210> 6
 <211> 763
 <212> PRT
 <213> Arabidopsis thaliana

<400> 6
 Gly Ile Ile Asn Gly Pro Lys Arg Glu Arg Ser Tyr Lys Val Ala Ile
 1 5 10 15
 Lys Phe Val Ala Arg Ala Asn Met His His Leu Gly Glu Phe Leu Ala
 20 25 30
 Gly Lys Arg Ala Asp Cys Pro Gln Glu Ala Val Gln Ile Leu Asp Ile
 35 40 45
 Val Leu Arg Glu Leu Ser Val Lys Arg Phe Cys Pro Val Gly Arg Ser
 50 55 60
 Phe Phe Ser Pro Asp Ile Lys Thr Pro Gln Arg Leu Gly Glu Gly Leu

65					70					75				80
Glu	Ser	Trp	Cys	Gly	Phe	Tyr	Gln	Ser	Ile	Arg	Pro	Thr	Gln	Met Gly
				85					90					95
Leu	Ser	Leu	Asn	Ile	Asp	Met	Ala	Ser	Ala	Ala	Phe	Ile	Glu	Pro Leu
			100					105					110	
Pro	Val	Ile	Glu	Phe	Val	Ala	Gln	Leu	Leu	Gly	Lys	Asp	Val	Leu Ser
			115				120					125		
Lys	Pro	Leu	Ser	Asp	Ser	Asp	Arg	Val	Lys	Ile	Lys	Lys	Gly	Leu Arg
			130			135					140			
Gly	Val	Lys	Val	Glu	Val	Thr	His	Arg	Ala	Asn	Val	Arg	Arg	Lys Tyr
145					150					155				160
Arg	Val	Ala	Gly	Leu	Thr	Thr	Gln	Pro	Thr	Arg	Glu	Leu	Met	Phe Pro
				165					170					175
Val	Asp	Glu	Asn	Cys	Thr	Met	Lys	Ser	Val	Ile	Glu	Tyr	Phe	Gln Glu
			180					185					190	
Met	Tyr	Gly	Phe	Thr	Ile	Gln	His	Thr	His	Leu	Pro	Cys	Leu	Gln Val
			195			200						205		
Gly	Asn	Gln	Lys	Lys	Ala	Ser	Tyr	Leu	Pro	Met	Glu	Ala	Cys	Lys Ile
			210			215					220			
Val	Glu	Gly	Gln	Arg	Tyr	Thr	Lys	Arg	Leu	Asn	Glu	Lys	Gln	Ile Thr
225				230						235				240
Ala	Leu	Leu	Lys	Val	Thr	Cys	Gln	Arg	Ala	Glu	Gly	Gln	Arg	Asn Asp
				245					250					255
Ile	Leu	Arg	Thr	Val	Gln	His	Asn	Ala	Tyr	Asp	Gln	Asp	Pro	Tyr Ala
			260					265					270	
Lys	Glu	Phe	Gly	Met	Asn	Ile	Ser	Glu	Lys	Leu	Ala	Ser	Val	Glu Ala
			275				280						285	
Arg	Ile	Leu	Pro	Ala	Pro	Trp	Leu	Lys	Tyr	His	Glu	Asn	Gly	Lys Glu
			290			295					300			
Lys	Asp	Cys	Leu	Pro	Gln	Val	Gly	Gln	Trp	Asn	Met	Met	Asn	Lys Lys
305					310					315				320
Met	Ile	Asn	Gly	Met	Thr	Val	Ser	Arg	Trp	Ala	Cys	Val	Asn	Phe Ser
				325					330					335
Arg	Ser	Val	Gln	Glu	Asn	Val	Ala	Arg	Gly	Phe	Cys	Asn	Glu	Leu Gly
			340					345					350	
Gln	Met	Cys	Glu	Val	Ser	Gly	Met	Glu	Phe	Asn	Pro	Glu	Pro	Val Ile
			355				360					365		
Pro	Ile	Tyr	Ser	Ala	Arg	Pro	Asp	Gln	Val	Glu	Lys	Ala	Leu	Lys His
						375						380		
Val	Tyr	His	Thr	Ser	Met	Asn	Lys	Thr	Lys	Gly	Lys	Glu	Leu	Glu Leu
385					390					395				400
Leu	Leu	Ala	Ile	Leu	Pro	Asp	Asn	Asn	Gly	Ser	Leu	Tyr	Gly	Asp Leu
				405					410					415
Lys	Arg	Ile	Cys	Glu	Thr	Glu	Leu	Gly	Leu	Ile	Ser	Gln	Cys	Cys Leu
			420					425					430	
Thr	Lys	His	Val	Phe	Lys	Ile	Ser	Lys	Gln	Tyr	Leu	Ala	Asp	Val Ser
			435				440					445		
Leu	Lys	Ile	Asn	Val	Lys	Met	Gly	Gly	Arg	Asn	Thr	Val	Leu	Val Asp
						455						460		
Ala	Ile	Ser	Cys	Arg	Ile	Pro	Leu	Val	Ser	Asp	Ile	Pro	Thr	Ile Ile
465					470					475				480
Phe	Gly	Ala	Asp	Val	Thr	His	Pro	Glu	Asn	Gly	Glu	Glu	Ser	Ser Pro
				485					490					495
Ser	Ile	Ala	Ala	Val	Val	Ala	Ser	Gln	Asp	Trp	Pro	Glu	Val	Thr Lys
			500					505					510	
Tyr	Ala	Gly	Leu	Val	Cys	Ala	Gln	Ala	His	Arg	Gln	Glu	Leu	Ile Gln
			515				520					525		
Asp	Leu	Tyr	Lys	Thr	Trp	Gln	Asp	Pro	Val	Arg	Gly	Thr	Val	Ser Gly
			530			535					540			
Gly	Met	Ile	Arg	Asp	Leu	Leu	Ile	Ser	Phe	Arg	Lys	Ala	Thr	Gly Gln
545					550					555				560

Pro	Asp	Arg	Arg	Ile	Glu	Arg	Leu	Arg	Met	Phe	Asn	Lys	Arg	Leu	Lys
225					230					235					240
Ser	Cys	Lys	Gln	Ser	Val	Glu	Thr	Leu	Lys	Ser	Trp	Asn	Ile	Glu	Leu
			245						250					255	
Asp	Ser	Ala	Leu	Val	Glu	Ile	Pro	Ala	Arg	Val	Leu	Pro	Pro	Glu	Lys
			260					265				270			
Ile	Leu	Phe	Gly	Asn	Gln	Lys	Ile	Phe	Val	Cys	Asp	Ala	Arg	Ala	Asp
		275					280					285			
Trp	Thr	Asn	Glu	Phe	Arg	Thr	Cys	Ser	Met	Phe	Lys	Asn	Val	His	Ile
	290					295					300				
Asn	Arg	Trp	Tyr	Val	Ile	Thr	Pro	Ser	Arg	Asn	Leu	Arg	Glu	Thr	Gln
305					310					315					320
Glu	Phe	Val	Gln	Met	Cys	Ile	Arg	Thr	Ala	Ser	Ser	Met	Lys	Met	Asn
				325					330					335	
Ile	Cys	Asn	Pro	Ile	Tyr	Glu	Glu	Ile	Pro	Asp	Asp	Arg	Asn	Gly	Thr
			340					345					350		
Tyr	Ser	Gln	Ala	Ile	Asp	Asn	Ala	Ala	Ala	Asn	Asp	Pro	Gln	Ile	Val
		355					360					365			
Met	Val	Val	Met	Arg	Ser	Pro	Asn	Glu	Glu	Lys	Tyr	Ser	Cys	Ile	Lys
	370					375						380			
Lys	Arg	Thr	Cys	Val	Asp	Arg	Pro	Val	Pro	Ser	Gln	Val	Val	Thr	Leu
385					390					395					400
Lys	Val	Ile	Ala	Pro	Arg	Gln	Gln	Lys	Pro	Thr	Gly	Leu	Met	Ser	Ile
				405					410					415	
Ala	Thr	Lys	Val	Val	Ile	Gln	Met	Asn	Ala	Lys	Leu	Met	Gly	Ala	Pro
			420					425					430		
Trp	Gln	Val	Val	Ile	Pro	Leu	His	Gly	Leu	Met	Thr	Val	Gly	Phe	Asp
		435					440						445		
Val	Cys	His	Ser	Pro	Lys	Asn	Lys	Asn	Lys	Ser	Tyr	Gly	Ala	Phe	Val
	450					455					460				
Ala	Thr	Met	Asp	Gln	Lys	Glu	Ser	Phe	Arg	Tyr	Phe	Ser	Thr	Val	Asn
465					470					475					480
Glu	His	Ile	Lys	Gly	Gln	Glu	Leu	Ser	Glu	Gln	Met	Ser	Val	Asn	Met
				485					490					495	
Ala	Cys	Ala	Leu	Arg	Ser	Tyr	Gln	Glu	Gln	His	Arg	Ser	Leu	Pro	Glu
			500					505					510		
Arg	Ile	Leu	Phe	Phe	Arg	Asp	Gly	Val	Gly	Asp	Gly	Gln	Leu	Tyr	Gln
		515					520						525		
Val	Val	Asn	Ser	Glu	Val	Asn	Thr	Leu	Lys	Asp	Arg	Leu	Asp	Glu	Ile
	530					535					540				
Tyr	Lys	Ser	Ala	Gly	Lys	Gln	Glu	Gly	Cys	Arg	Met	Thr	Phe	Ile	Ile
545					550					555					560
Val	Ser	Lys	Arg	Ile	Asn	Ser	Arg	Tyr	Phe	Thr	Gly	His	Arg	Asn	Pro
				565					570					575	
Val	Pro	Gly	Thr	Val	Val	Asp	Asp	Val	Ile	Thr	Leu	Pro	Glu	Arg	Tyr
			580					585					590		
Asp	Phe	Phe	Leu	Val	Ser	Gln	Ala	Val	Arg	Ile	Gly	Thr	Val	Ser	Pro
		595					600					605			
Thr	Ser	Tyr	Asn	Val	Ile	Ser	Asp	Asn	Met	Gly	Leu	Asn	Ala	Asp	Lys
	610					615					620				
Leu	Gln	Met	Leu	Ser	Tyr	Lys	Met	Thr	His	Met	Tyr	Tyr	Asn	Tyr	Ser
625					630					635					640
Gly	Thr	Ile	Arg	Val	Pro	Ala	Val	Cys	His	Tyr	Ala	His	Lys	Leu	Ala
				645					650					655	
Phe	Leu	Val	Ala	Glu	Ser	Ile	Asn	Arg	Ala	Pro	Ser	Ala	Gly	Leu	Gln
			660					665					670		
Asn	Gln	Leu	Tyr	Phe	Leu										
			675												

<210> 8

<211> 69

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Consensus sequence

 <221> VARIANT
 <222> <222> 2, 3, 4, 6, 8, 9, 12, 13, 14, 15, 16, 17, 18, 19, 21,
 22, 23, 24, 26, 29, 31, 32, 33, 35, 36, 37, 39, 40,
 41, 44, 45, 46, 47, 49, 51, 55, 56, 59, 60, 63, 64,
 67, 68

 <223> Xaa = Any Amino Acid

 <221> VARIANT
 <222> 10, 25, 43

 <223> Xaa = Any amino Acid if present

 <400> 8
 Pro Xaa Xaa Xaa Leu Xaa Glu Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Gly Pro Xaa His Xaa Xaa
 20 25 30
 Xaa Phe Xaa Xaa Xaa Val Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Gly
 35 40 45
 Xaa Gly Xaa Ser Lys Lys Xaa Xaa Ala Lys Xaa Xaa Ala Ala Xaa Xaa
 50 55 60
 Ala Leu Xaa Xaa Leu
 65

 <210> 9
 <211> 766
 <212> PRT
 <213> Caenorhabditis elegans

 <400> 9
 Ser Ala Val Glu Arg Gln Phe Ser Val Ser Leu Lys Trp Val Gly Gln
 1 5 10 15
 Val Ser Leu Ser Thr Leu Glu Asp Ala Met Glu Gly Arg Val Arg Gln
 20 25 30
 Val Pro Phe Glu Ala Val Gln Ala Met Asp Val Ile Leu Arg His Leu
 35 40 45
 Pro Ser Leu Lys Tyr Thr Pro Val Gly Arg Ser Phe Phe Ser Pro Pro
 50 55 60
 Val Pro Asn Ala Ser Gly Val Met Ala Gly Ser Cys Pro Pro Gln Ala
 65 70 75 80
 Ser Gly Ala Val Ala Gly Gly Ala His Ser Ala Gly Gln Tyr His Ala
 85 90 95
 Glu Ser Lys Leu Gly Gly Gly Arg Glu Val Trp Phe Gly Phe His Gln
 100 105 110
 Ser Val Arg Pro Ser Gln Trp Lys Met Met Leu Asn Ile Asp Val Ser
 115 120 125
 Ala Thr Ala Phe Tyr Arg Ser Met Pro Val Ile Glu Phe Ile Ala Glu
 130 135 140
 Val Leu Glu Leu Pro Val Gln Ala Leu Ala Glu Arg Arg Ala Leu Ser
 145 150 155 160
 Asp Ala Gln Arg Val Lys Phe Thr Lys Glu Ile Arg Gly Leu Lys Ile
 165 170 175
 Glu Ile Thr His Cys Gly Gln Met Arg Arg Lys Tyr Arg Val Cys Asn
 180 185 190

Val	Thr	Arg	Arg	Pro	Ala	Gln	Thr	Gln	Thr	Phe	Pro	Leu	Gln	Leu	Glu
		195					200					205			
Thr	Gly	Gln	Thr	Ile	Glu	Cys	Thr	Val	Ala	Lys	Tyr	Phe	Tyr	Asp	Lys
	210					215					220				
Tyr	Arg	Ile	Gln	Leu	Lys	Tyr	Pro	His	Leu	Pro	Cys	Leu	Gln	Val	Gly
225					230					235					240
Gln	Glu	Gln	Lys	His	Thr	Tyr	Leu	Pro	Pro	Glu	Val	Cys	Asn	Ile	Val
				245					250					255	
Pro	Gly	Gln	Arg	Cys	Ile	Lys	Lys	Leu	Thr	Asp	Val	Gln	Thr	Ser	Thr
			260					265					270		
Met	Ile	Lys	Ala	Thr	Ala	Arg	Ser	Ala	Pro	Glu	Arg	Glu	Arg	Glu	Ile
		275					280					285			
Ser	Asn	Leu	Val	Arg	Lys	Ala	Glu	Phe	Ser	Ala	Asp	Pro	Phe	Ala	His
	290					295					300				
Glu	Phe	Gly	Ile	Thr	Ile	Asn	Pro	Ala	Met	Thr	Glu	Val	Lys	Gly	Arg
305					310					315					320
Val	Leu	Ser	Ala	Pro	Lys	Leu	Leu	Tyr	Gly	Gly	Arg	Thr	Arg	Ala	Thr
				325					330					335	
Ala	Leu	Pro	Asn	Gln	Gly	Val	Trp	Asp	Met	Arg	Gly	Lys	Gln	Phe	His
			340					345					350		
Thr	Gly	Ile	Asp	Val	Arg	Val	Trp	Ala	Ile	Ala	Cys	Phe	Ala	Gln	Gln
		355					360					365			
Gln	His	Val	Lys	Glu	Asn	Asp	Leu	Arg	Met	Phe	Thr	Asn	Gln	Leu	Gln
	370					375					380				
Arg	Ile	Ser	Asn	Asp	Ala	Gly	Met	Pro	Ile	Val	Gly	Asn	Pro	Cys	Phe
385					390					395					400
Cys	Lys	Tyr	Ala	Val	Gly	Val	Glu	Gln	Val	Glu	Pro	Met	Phe	Lys	Tyr
				405					410					415	
Leu	Lys	Gln	Asn	Tyr	Ser	Gly	Ile	Gln	Leu	Val	Val	Val	Val	Leu	Pro
			420					425					430		
Gly	Lys	Thr	Pro	Val	Tyr	Ala	Glu	Val	Lys	Arg	Val	Gly	Asp	Thr	Val
		435					440					445			
Leu	Gly	Ile	Ala	Thr	Gln	Cys	Val	Gln	Ala	Lys	Asn	Ala	Ile	Arg	Thr
	450					455					460				
Thr	Pro	Gln	Thr	Leu	Ser	Asn	Leu	Cys	Leu	Lys	Met	Asn	Val	Lys	Leu
465					470					475					480
Gly	Gly	Val	Asn	Ser	Ile	Leu	Leu	Pro	Asn	Val	Arg	Pro	Arg	Ile	Phe
				485					490					495	
Asn	Glu	Pro	Val	Ile	Phe	Phe	Gly	Cys	Asp	Ile	Thr	His	Pro	Pro	Ala
			500					505					510		
Gly	Asp	Ser	Arg	Lys	Pro	Ser	Ile	Ala	Ala	Val	Val	Gly	Ser	Met	Asp
		515					520					525			
Ala	His	Pro	Ser	Arg	Tyr	Ala	Ala	Thr	Val	Arg	Val	Gln	Gln	His	Arg
	530					535					540				
Gln	Glu	Ile	Ile	Ser	Asp	Leu	Thr	Tyr	Met	Val	Arg	Glu	Leu	Leu	Val
545					550					555					560
Gln	Phe	Tyr	Arg	Asn	Thr	Arg	Phe	Lys	Pro	Ala	Arg	Ile	Val	Val	Tyr
				565					570					575	
Arg	Asp	Gly	Val	Ser	Glu	Gly	Gln	Phe	Phe	Asn	Val	Leu	Gln	Tyr	Glu
			580					585					590		
Leu	Arg	Ala	Ile	Arg	Glu	Ala	Cys	Met	Met	Leu	Glu	Arg	Gly	Tyr	Gln
		595					600					605			
Pro	Gly	Ile	Thr	Phe	Ile	Ala	Val	Gln	Lys	Arg	His	His	Thr	Arg	Leu
	610					615					620				
Phe	Ala	Val	Asp	Lys	Lys	Asp	Gln	Val	Gly	Lys	Ala	Tyr	Asn	Ile	Pro
625					630					635					640
Pro	Gly	Thr	Thr	Val	Asp	Val	Gly	Ile	Thr	His	Pro	Thr	Glu	Phe	Asp
				645					650					655	
Phe	Tyr	Leu	Cys	Ser	His	Ala	Gly	Ile	Gln	Gly	Thr	Ser	Arg	Pro	Ser
			660					665					670		
His	Tyr	His	Val	Leu	Trp	Asp	Asp	Asn	Asn	Leu	Thr	Ala	Asp	Glu	Leu

			20						25				30				
Phe	Thr	Ile	Thr	Cys	Arg	Val	Glu	Thr	Phe	Val	Glu	Thr	Gly	Ser	Gly		
		35					40					45					
Thr	Ser	Lys	Gln	Val	Ala	Lys	Arg	Val	Ala	Ala	Glu	Lys	Leu	Leu	Thr		
	50					55					60						
Lys	Phe																
65																	

<210> 12
 <211> 66
 <212> PRT
 <213> Homo sapiens

Phe	Met	Glu	Glu	Leu	Asn	Thr	Tyr	Arg	Gln	Lys	Gln	Gly	Val	Val	Leu		
1				5					10					15			
Lys	Tyr	Gln	Glu	Leu	Pro	Asn	Ser	Gly	Pro	Pro	His	Asp	Arg	Arg	Phe		
		20						25				30					
Thr	Phe	Gln	Val	Ile	Ile	Asp	Gly	Arg	Glu	Phe	Pro	Glu	Gly	Glu	Gly		
	35					40						45					
Arg	Ser	Lys	Lys	Glu	Ala	Lys	Asn	Ala	Ala	Ala	Lys	Leu	Ala	Val	Glu		
	50					55					60						
Ile	Leu																
65																	

<210> 13
 <211> 818
 <212> PRT
 <213> Caenorhabditis elegans

Val	Asn	Glu	Glu	Ile	Lys	Val	Gln	Phe	Ala	Lys	Asn	Phe	Val	Tyr	Asp		
1				5				10						15			
Asn	Asn	Ser	Ile	Leu	Arg	Val	Pro	Glu	Ser	Phe	His	Asp	Pro	Asn	Arg		
		20						25				30					
Phe	Glu	Gln	Ser	Leu	Glu	Val	Ala	Pro	Arg	Ile	Glu	Ala	Trp	Phe	Gly		
	35					40					45						
Ile	Tyr	Ile	Gly	Ile	Lys	Glu	Leu	Phe	Asp	Gly	Glu	Pro	Val	Leu	Asn		
	50				55					60							
Phe	Ala	Ile	Val	Asp	Lys	Leu	Phe	Tyr	Asn	Ala	Pro	Lys	Met	Ser	Leu		
65				70				75						80			
Leu	Asp	Tyr	Leu	Leu	Ile	Val	Asp	Pro	Gln	Ser	Cys	Asn	Asp	Asp			
			85					90					95				
Val	Arg	Lys	Asp	Leu	Lys	Thr	Lys	Leu	Met	Ala	Gly	Lys	Met	Thr	Ile		
		100					105						110				
Arg	Gln	Ala	Ala	Arg	Pro	Arg	Ile	Arg	Gln	Leu	Leu	Glu	Asn	Leu	Lys		
	115					120						125					
Leu	Lys	Cys	Ala	Glu	Val	Trp	Asp	Asn	Glu	Met	Ser	Arg	Leu	Thr	Glu		
	130				135					140							
Arg	His	Leu	Thr	Phe	Leu	Asp	Leu	Cys	Glu	Glu	Asn	Ser	Leu	Val	Tyr		
145				150				155						160			
Lys	Val	Thr	Gly	Lys	Ser	Asp	Arg	Gly	Arg	Asn	Ala	Lys	Lys	Tyr	Asp		
		165					170						175				
Thr	Thr	Leu	Phe	Lys	Ile	Tyr	Glu	Glu	Asn	Lys	Lys	Phe	Ile	Glu	Phe		
		180					185						190				
Pro	His	Leu	Pro	Leu	Val	Lys	Val	Lys	Ser	Gly	Ala	Lys	Glu	Tyr	Ala		
		195				200						205					
Val	Pro	Met	Glu	His	Leu	Glu	Val	His	Glu	Lys	Pro	Gln	Arg	Tyr	Lys		
	210				215						220						
Asn	Arg	Ile	Asp	Leu	Val	Met	Gln	Asp	Lys	Phe	Leu	Lys	Arg	Ala	Thr		
225					230					235					240		

Arg	Lys	Pro	His	Asp	Tyr	Lys	Glu	Asn	Thr	Leu	Lys	Met	Leu	Lys	Glu	245	250	255
Leu	Asp	Phe	Ser	Ser	Glu	Glu	Leu	Asn	Phe	Val	Glu	Arg	Phe	Gly	Leu	260	265	270
Cys	Ser	Lys	Leu	Gln	Met	Ile	Glu	Cys	Pro	Gly	Lys	Val	Leu	Lys	Glu	275	280	285
Pro	Met	Leu	Val	Asn	Ser	Val	Asn	Glu	Gln	Ile	Lys	Met	Thr	Pro	Val	290	295	300
Ile	Arg	Gly	Phe	Gln	Glu	Lys	Gln	Leu	Asn	Val	Val	Pro	Glu	Lys	Glu	305	310	315
Leu	Cys	Cys	Ala	Val	Phe	Val	Val	Asn	Glu	Thr	Ala	Gly	Asn	Pro	Cys	325	330	335
Leu	Glu	Glu	Asn	Asp	Val	Val	Lys	Phe	Tyr	Thr	Glu	Leu	Ile	Gly	Gly	340	345	350
Cys	Lys	Phe	Arg	Gly	Ile	Arg	Ile	Gly	Ala	Asn	Glu	Asn	Arg	Gly	Ala	355	360	365
Gln	Ser	Ile	Met	Tyr	Asp	Ala	Thr	Lys	Asn	Glu	Tyr	Ala	Phe	Tyr	Lys	370	375	380
Asn	Cys	Thr	Leu	Asn	Thr	Gly	Ile	Gly	Arg	Phe	Glu	Ile	Ala	Ala	Thr	385	390	395
Glu	Ala	Lys	Asn	Met	Phe	Glu	Arg	Leu	Pro	Asp	Lys	Glu	Gln	Lys	Val	405	410	415
Leu	Met	Phe	Ile	Ile	Ile	Ser	Lys	Arg	Gln	Leu	Asn	Ala	Tyr	Gly	Phe	420	425	430
Val	Lys	His	Tyr	Cys	Asp	His	Thr	Ile	Gly	Val	Ala	Asn	Gln	His	Ile	435	440	445
Thr	Ser	Glu	Thr	Val	Thr	Lys	Ala	Leu	Ala	Ser	Leu	Arg	His	Glu	Lys	450	455	460
Gly	Ser	Lys	Arg	Ile	Phe	Tyr	Gln	Ile	Ala	Leu	Lys	Ile	Asn	Ala	Lys	465	470	475
Leu	Gly	Gly	Ile	Asn	Gln	Glu	Leu	Asp	Trp	Ser	Glu	Ile	Ala	Glu	Ile	485	490	495
Ser	Pro	Glu	Glu	Lys	Glu	Arg	Arg	Lys	Thr	Met	Pro	Leu	Thr	Met	Tyr	500	505	510
Val	Gly	Ile	Asp	Val	Thr	His	Pro	Thr	Ser	Tyr	Ser	Gly	Ile	Asp	Tyr	515	520	525
Ser	Ile	Ala	Ala	Val	Val	Ala	Ser	Ile	Asn	Pro	Gly	Gly	Thr	Ile	Tyr	530	535	540
Arg	Asn	Met	Ile	Val	Thr	Gln	Glu	Glu	Cys	Arg	Pro	Gly	Glu	Arg	Ala	545	550	555
Val	Ala	His	Gly	Arg	Glu	Arg	Thr	Asp	Ile	Leu	Glu	Ala	Lys	Phe	Val	565	570	575
Lys	Leu	Leu	Arg	Glu	Phe	Ala	Glu	Asn	Asn	Asp	Asn	Arg	Ala	Pro	Ala	580	585	590
His	Ile	Val	Val	Tyr	Arg	Asp	Gly	Val	Ser	Asp	Ser	Glu	Met	Leu	Arg	595	600	605
Val	Ser	His	Asp	Glu	Leu	Arg	Ser	Leu	Lys	Ser	Glu	Val	Lys	Gln	Phe	610	615	620
Met	Ser	Glu	Arg	Asp	Gly	Glu	Asp	Pro	Glu	Pro	Lys	Tyr	Thr	Phe	Ile	625	630	635
Val	Ile	Gln	Lys	Arg	His	Asn	Thr	Arg	Leu	Leu	Arg	Arg	Met	Glu	Lys	645	650	655
Asp	Lys	Pro	Val	Val	Asn	Lys	Asp	Leu	Thr	Pro	Ala	Glu	Thr	Asp	Val	660	665	670
Ala	Val	Ala	Ala	Val	Lys	Gln	Trp	Glu	Glu	Asp	Met	Lys	Glu	Ser	Lys	675	680	685
Glu	Thr	Gly	Ile	Val	Asn	Pro	Ser	Ser	Gly	Thr	Thr	Val	Asp	Lys	Leu	690	695	700
Ile	Val	Ser	Lys	Tyr	Lys	Phe	Asp	Phe	Phe	Leu	Ala	Ser	His	His	Gly	705	710	715
Val	Leu	Gly	Thr	Ser	Arg	Pro	Gly	His	Tyr	Thr	Val	Met	Tyr	Asp	Asp	720		

725 730 735
 Lys Gly Met Ser Gln Asp Glu Val Tyr Lys Met Thr Tyr Gly Leu Ala
 740 745 750
 Phe Leu Ser Ala Arg Cys Arg Lys Pro Ile Ser Leu Pro Val Pro Val
 755 760 765
 His Tyr Ala His Leu Ser Cys Glu Lys Ala Lys Glu Leu Tyr Arg Thr
 770 775 780
 Tyr Lys Glu His Tyr Ile Gly Asp Tyr Ala Gln Pro Arg Thr Arg His
 785 790 795 800
 Glu Met Glu His Phe Leu Gln Thr Asn Val Lys Tyr Pro Gly Met Ser
 805 810 815
 Phe Ala

<210> 14
 <211> 63
 <212> PRT
 <213> Caenorhabditis elegans

<400> 14
 Trp Val Gly Lys Leu Gln Phe Lys Ser Gln Lys Ser Lys Leu Gln Ala
 1 5 10 15
 Asp Ile Tyr Glu Asp Ser Lys Asn Glu Arg Thr Glu Phe Thr Leu Val
 20 25 30
 Ile Cys Thr Met Cys Asn Gln Lys Thr Arg Gly Ile Thr Ser Lys Gln
 35 40 45
 Lys Asp Ala Lys Asn Leu Ala Ala Trp Leu Met Trp Lys Ala Leu
 50 55 60